

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: January 3, 2002, 23:06:20 ; Search time 56.46 Seconds  
(without alignments)  
2391.239 Million cell updates/sec

Title: US-09-497-822a-19  
Perfect score: 4912  
Sequence: 1 MEVQLGLGRVYPPPSKTYR.....SVQVPKILSGKVKPIYFHTQ 923

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues  
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_17:\*
- 1: sp-archaea:\*
  - 2: sp-bacteria:\*
  - 3: sp-fungi:\*
  - 4: sp-human:\*
  - 5: sp-invertebrate:\*
  - 6: sp-mammal:\*
  - 7: sp-mhc:\*
  - 8: sp-organelle:\*
  - 9: sp-phage:\*
  - 10: sp-plant:\*
  - 11: sp-rodent:\*
  - 12: sp-virus:\*
  - 13: sp-vertebrate:\*
  - 14: sp-unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4777.5	97.3	906	Q9UN21	Q9UN21 homo sapien
2	4341.5	88.4	896	Q9GKL7	Q9GKL7 sus scrofa
3	4298	87.5	895	Q9GKN9	Q9GKN9 sus scrofa
4	3822.5	77.8	730	Q13771	Q13771 homo sapien
5	2873	58.5	544	Q9BZG7	Q9BZG7 homo sapien
6	2857	58.2	542	Q9BZG6	Q9BZG6 homo sapien
7	2846.5	57.9	539	Q9NUA2	Q9NUA2 homo sapien
8	2802.5	57.1	531	Q9BZG5	Q9BZG5 homo sapien
9	2414.5	49.2	780	P70048	P70048 xenopus lae
10	1676	34.1	344	Q91445	Q91445 serinus can
11	1639.5	33.4	853	Q93245	Q93245 oncorhynch
12	1604	32.7	803	Q97684	Q97684 ovis aries
13	1600	32.6	769	Q93497	Q93497 pagrus majo
14	1556	31.7	797	Q9PWG5	Q9PWG5 anguilla ja
15	1532	31.2	848	Q93244	Q93244 oncorhynch
16	1472.5	30.0	563	Q9YGV9	Q9YGV9 anguilla ja
17	1270	25.9	939	Q9DDJ4	Q9DDJ4 halichoeres
18	1180.5	24.0	692	Q9GLWQ	Q9GLWQ canis fami
19				Q9W6F4	Q9W6F4 haplochromi

20	1179	24.0	732	13	Q9DDU9
21	1157.5	23.6	583	13	Q9DEV4
22	1150	23.4	232	13	Q9IA30
23	1125	22.9	710	13	Q9IBD5
24	1064.5	21.7	360	13	Q42274
25	1055	21.5	982	6	Q9N0W8
26	978	19.9	232	6	Q9BE98
27	966	19.7	348	13	Q91425
28	892	18.2	359	13	Q9IAC6
29	816	16.6	298	6	Q28547
30	725.5	14.8	200	13	Q9I8F5
31	715	14.6	166	13	Q91698
32	627	12.8	133	13	Q91426
33	590	12.0	258	6	Q9BDJ7
34	577	11.7	117	6	Q18925
35	569	11.6	196	6	Q18991
36	568	11.6	110	6	Q97891
37	479	9.8	169	11	Q63879
38	461	9.4	569	13	Q98SM9
39	458	9.3	91	6	Q18928
40	451	9.2	95	6	Q97608
41	444	9.0	95	6	Q97667
42	443	9.0	526	6	Q9BDW5
43	435	8.9	95	6	Q97622
44	417.5	8.5	484	5	Q9VSE9
45	410	8.3	125	6	Q18972

ALIGNMENTS

RESULT 1  
Q9UN21 ID Q9UN21 PRELIMINARY; PRT; 906 AA.  
AC Q9UN21;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DI ANDROGEN RECEPTOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MAMMARY CARCINOMA;  
RA Jin C.H., Urcan-Biseli M.S., Schrader W.T.;  
RT "Androgen receptor sequences in human mammary carcinoma MDA-MB-453 cells."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.  
DR EMBL; AF162704; AD45921.1; -;  
DR HSSP; P06536; IGDC.  
DR InterPro; IPR001103; Androgen\_recep.  
DR InterPro; IPR000536; Hormone\_rec\_lig.  
DR InterPro; IPR001628; zf-C4.  
DR Pfam; PF02166; Androgen\_recep; 1.  
DR Pfam; PF00104; hormone\_rec; 1.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PRO0047; STROIDFINGER.  
DR SMART; SM00430; HOLI; 1.  
DR SMART; SM00399; ZnF\_C4; 1.  
DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
KW Zinc-finger.  
SQ SEQUENCE 906 AA; 97884 MW; 0A1FA8802B2EDDAF CRC64;

Query Match 97.3%  
Best Local Similarity 97.8%  
Matches 903; Conservative 1; Mismatches 2; Indels 17; Gaps 2;

Sus scrofa (Pig).  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
NCBI\_TaxID=9823;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=PITUITARY;  
Song J.H., Fahrénkrug S.C., Rohrer G.A., Wise T.H., Ford J.J.;  
"Sus scrofa androgen receptor (AR) coding sequence."  
Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
[2]  
SEQUENCE FROM N.A.  
TISSUE=PITUITARY;  
Song J.H., Fahrénkrug S.C., Rohrer G.A., Wise T.H., Ford J.J.;  
"Porcine androgen receptor (AR) cDNA cloning: Expression in pituitary  
associates with FSH secretion in boars."  
Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
-1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.  
EMBL: AF02775; AAC37994.1;  
InterPro: IPR001103; Androgen\_recep.  
InterPro: IPR000536; Hormone\_rec\_lig.  
InterPro: IPR001628; zf-C4.  
Pfam: PF02166; Androgen\_recep; 1.  
Pfam: PF00104; Hormone\_rec; 1.  
Pfam: PF00105; zf-C4; 1.  
PRINTS: PR00047; STROIDFINGER.  
SMART: SM00430; HOLI; 1.  
SMART: SM00399; ZnF\_C4; 1.  
PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1.  
DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
zinc-finger.  
SEQUENCE 896 AA: 97094 MW: 4405F6E73BDC796 CRC64;

[illegible]





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Db 421 AGAAGCGSGPSAAASSSWHTLFTAEAGLYGPGCGGGGGGGGGGGGGGGGGEA 480
QY 479 GAVAPGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVYPSPTCKSEMGPWMDSYSGPY 538
Db 481 GAVAPGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVYPSPTCKSEMGPWMDSYSGPY 540
QY 539 GDMR 542
Db 541 GDMR 544

RESULT 6
Q9BZG6
ID Q9BZG6 PRELIMINARY; PRT; 542 AA.
AC Q9BZG6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ANDROGEN RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Magklara A., Diamandis E.P.;
RT "Poly-Q and poly-G repeats in the androgen receptor of the breast
cancer cell line BT-20A.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321915; AAK09425.1;
FT Receptor.
KW NON_TER 542 542
SQ SEQUENCE 542 AA; 53628 MW; C363EF841CAF7739 CRC64;

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Query Match 58.2%; Score 2857; DB 4; Length 542;
Best Local Similarity 99.6%; Pred. No. 1.3e-206;
Matches 541; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MEVOLGLGRVYPRPPSKTYRGAFONLFQSVREVIONPGPRHPEAASAPPGASLILL--QQ 59
Db 1 MEVOLGLGRVYPRPPSKTYRGAFONLFQSVREVIONPGPRHPEAASAPPGASLILL--QQ 60
QY 60 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 119
Db 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 120
QY 120 PQSALECHPERGCVPEPAAVAAASKGLPQLPAPPPDEDDSAAPSTLSLLGPTFFGLSSC 179
Db 121 PQSALECHPERGCVPEPAAVAAASKGLPQLPAPPPDEDDSAAPSTLSLLGPTFFGLSSC 180
QY 180 SADLKDILSEASTMQLLQOQQQOQAVSEGSRRAREASGAPTSSKDNVYLGTTSTISDNK 239
Db 181 SADLKDILSEASTMQLLQOQQQOQAVSEGSRRAREASGAPTSSKDNVYLGTTSTISDNK 240
QY 240 ELKAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKSLDD 299
Db 241 ELKAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKSLDD 300
QY 300 SAGKSTEDTAESYSPFKGGYTKGLESGCGSAAAGSSGTLELPSTLSLYKSGALDEAA 359
Db 301 SAGKSTEDTAESYSPFKGGYTKGLESGCGSAAAGSSGTLELPSTLSLYKSGALDEAA 360
QY 360 AYQSRDYNYNPLALAGPPPPPPHARIKLENPLDYGSAWAAAAAACRYGDLASLHGA 419
Db 361 AYQSRDYNYNPLALAGPPPPPPHARIKLENPLDYGSAWAAAAAACRYGDLASLHGA 420
QY 420 GAAGCGSGPSAAASSSWHTLFTAEAGLYGPGCGGGGGGGGGGGGGGGGGGGEAG 479
Db 421 GAAGCGSGPSAAASSSWHTLFTAEAGLYGPGCGGGGGGGGGGGGGGGGGGGEAG 479
QY 480 AVAPGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVYPSPTCKSEMGPWMDSYSGPY 539

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Db 480 AVAPGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVYPSPTCKSEMGPWMDSYSGPY 539
QY 540 DMR 542
Db 540 DMR 542

RESULT 7
Q9NUA2
ID Q9NUA2 PRELIMINARY; PRT; 539 AA.
AC Q9NUA2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE DJB0804.1 (ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR))
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chapman J.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Magklara A., Diamandis E.P.;
RT "Poly-Q and poly-G repeats in the androgen receptor of the breast
cancer cell line T-47b.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049564; CAB87955.1;
DR EMBL; AF321915; AAK09424.1;
DR InterPro; IPR001103; Androgen_recep.
DR Pfam; PF02166; Androgen_recep; 1.
KW NON_TER 539 539
SQ SEQUENCE 539 AA; 55444 MW; AB493953B89D869F CRC64;

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Query Match 57.9%; Score 2846.5; DB 4; Length 539;
Best Local Similarity 99.4%; Pred. No. 8.2e-206;
Matches 539; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

QY 1 MEVOLGLGRVYPRPPSKTYRGAFONLFQSVREVIONPGPRHPEAASAPPGASLILL--Q 60
Db 1 MEVOLGLGRVYPRPPSKTYRGAFONLFQSVREVIONPGPRHPEAASAPPGASLILL--Q 58
QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 120
Db 59 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 118
QY 121 PQSALECHPERGCVPEPAAVAAASKGLPQLPAPPPDEDDSAAPSTLSLLGPTFFGLSSC 180
Db 119 PQSALECHPERGCVPEPAAVAAASKGLPQLPAPPPDEDDSAAPSTLSLLGPTFFGLSSC 178
QY 181 ADLKDILSEASTMQLLQOQQQOQAVSEGSRRAREASGAPTSSKDNVYLGTTSTISDNK 240
Db 179 ADLKDILSEASTMQLLQOQQQOQAVSEGSRRAREASGAPTSSKDNVYLGTTSTISDNK 238
QY 241 LCKAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKSLDD 300
Db 239 LCKAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKSLDD 298
QY 301 SAGKSTEDTAESYSPFKGGYTKGLESGCGSAAAGSSGTLELPSTLSLYKSGALDEAA 360
Db 299 SAGKSTEDTAESYSPFKGGYTKGLESGCGSAAAGSSGTLELPSTLSLYKSGALDEAA 358
QY 361 YQSRDYNYNPLALAGPPPPPPHARIKLENPLDYGSAWAAAAAACRYGDLASLHGA 420
Db 359 YQSRDYNYNPLALAGPPPPPPHARIKLENPLDYGSAWAAAAAACRYGDLASLHGA 418

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QY 481 VAPYGYTRPPQGLAGQESDFTAPDVWYPGMVSRVYPSPCTCKSEMPWMDSYSGPYGD 540  
 Db 470 VAPYGYTRPPQGLAGQESDFTAPDVWYPGMVSRVYPSPCTCKSEMPWMDSYSGPYGD 529  
 QY 541 MR 542  
 Db 530 MR 531

RESULT 9  
 P70048  
 ID P70048 PRELIMINARY; PRT: 790 AA.  
 AC P70048;  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE ANDROGEN RECEPTOR ALPHA ISOFORM.  
 GN XL ALPHA AR.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OC NCBI\_TaxID=8355;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE-93376782; PubMed=7690145;  
 RA Fischer L., Catz D., Kelley D.;  
 RT "An androgen receptor mRNA isoform associated with hormone-induced  
 cell proliferation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8254-8256 (1993).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE-95324753; PubMed=7601302;  
 RA Fischer L.M., Catz D., Kelley D.B.;  
 RT "Androgen-directed development of the xenopus laevis larynx: control  
 of androgen receptor expression and tissue differentiation.";  
 RL Dev. Biol. 170:115-126 (1995).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RP Kamenetz F.R., Catz D.S., Fischer L.M., Kelley D.B.;  
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RN SEQUENCE FROM N.A.  
 RP Kelley D.B., Kamenetz F.R., Kelley D.B., Badea T.C.;  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.  
 DR EMBL; U67129; AAC97386.1;  
 DR HSP; P65336; LGDC  
 DR InterPro; IPR001103; Androgen\_recep.  
 DR InterPro; IPR000536; Hormone\_rec\_lig.  
 DR InterPro; IPR001628; zf-C4.  
 DR Pfam; PF02166; Androgen\_recep; 3.  
 DR Pfam; PF00104; hormone\_rec; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; ZnF\_C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
 KW Zinc-finger.  
 SQ SEQUENCE 790 AA; 86973 MW; 9E7FC136CCCC3906 CRC64;

Query Match 49.2%; Score 2414.5; DB 13; Length 790;  
 Best Local Similarity 54.5%; Pred. No. 4.1e-173; Indels 209; Gaps 29;  
 Matches 523; Conservative 65; Mismatches 162;  
 QY 1 MEVQGLGVRYPSPKTYRGAFQNLFSQSVREVIONPGFHPPEAASAPPASLLILQQQ 60  
 Db 1 MEVHGLGVRYPSPKTYRGAFQNLFSQSVREVIONPGFHPPEAASAPPASLLILQQQ 51  
 QY 61 QQQ 120

QY 421 AAGPGSGPSAAASSSWHTLTAEEGQLYPCGGGGGGGGGGGGGGGGGGGGGGGGEAGA 480  
 Db 419 AAGPGSGPSAAASSSWHTLTAEEGQLYPCGGGGGGGGGGGGGGGGGGGGGGGGEAGA 477  
 QY 481 VAPYGYTRPPQGLAGQESDFTAPDVWYPGMVSRVYPSPCTCKSEMPWMDSYSGPYGD 540  
 Db 478 VAPYGYTRPPQGLAGQESDFTAPDVWYPGMVSRVYPSPCTCKSEMPWMDSYSGPYGD 537  
 QY 541 MR 542  
 Db 538 MR 539

RESULT 8  
 Q9BZG5  
 ID Q9BZG5 PRELIMINARY; PRT: 531 AA.  
 AC Q9BZG5;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE ANDROGEN RECEPTOR (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP Magliara A., Dimandis E.P.;  
 RT "Poly-Q and poly-G repeats in the androgen receptor of the breast  
 cancer cell line MCF-7.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF321947; AAK04476.1;  
 KW Receptor.  
 FT NON\_TER  
 SQ SEQUENCE 531 AA; 54419 MW; FA0D3AA60AC20DAB CRC64;

Query Match 57.1%; Score 2802.5; DB 4; Length 531;  
 Best Local Similarity 98.0%; Pred. No. 1.6e-202;  
 Matches 531; Conservative 0; Mismatches 0; Indels 11; Gaps 2;  
 QY 1 MEVQGLGVRYPSPKTYRGAFQNLFSQSVREVIONPGFHPPEAASAPPASLLILQQQ 60  
 Db 1 MEVQGLGVRYPSPKTYRGAFQNLFSQSVREVIONPGFHPPEAASAPPASLLILQQQ 57  
 QY 61 QQQ 120  
 Db 58 QQQ 110  
 QY 121 PQSALECHPERGCVPEPAAVAAKGLPOLPAPPEDEDDSAAPSTLSLLGPTFPGLSSCS 180  
 Db 111 PQSALECHPERGCVPEPAAVAAKGLPOLPAPPEDEDDSAAPSTLSLLGPTFPGLSSCS 170  
 QY 181 ADLKDLSEASTMQLLQOQQQAVSGSSSGRAREASGAPTSSKDNLYLGGTSTISDNAE 240  
 Db 171 ADLKDLSEASTMQLLQOQQQAVSGSSSGRAREASGAPTSSKDNLYLGGTSTISDNAE 230  
 QY 241 LCKAVSVMLGLVEALEHLSPLGDLRCDCMYAPLLGVPPAVRPTCAPLAECCKGSLDLS 300  
 Db 231 LCKAVSVMLGLVEALEHLSPLGDLRCDCMYAPLLGVPPAVRPTCAPLAECCKGSLDLS 290  
 QY 301 AGKSTEDTAESYSPKGYTKGLESGILGCGSAAAGSSGTLEPSTLSLYKSGALDEAAA 360  
 Db 291 AGKSTEDTAESYSPKGYTKGLESGILGCGSAAAGSSGTLEPSTLSLYKSGALDEAAA 350  
 QY 361 YQSRDYNYFLALAGAPPPPPPPHARIKLENPLDYGSAWAAAAOCHYGLASLHGAG 420  
 Db 351 YQSRDYNYFLALAGAPPPPPPPHARIKLENPLDYGSAWAAAAOCHYGLASLHGAG 410  
 QY 421 AAGPGSGPSAAASSSWHTLTAEEGQLYPCGGGGGGGGGGGGGGGGGGGGGGGGEAGA 480  
 Db 411 AAGPGSGPSAAASSSWHTLTAEEGQLYPCGGGGGGGGGGGGGGGGGGGGGGGGEAGA 469

	NCBI_TaxID=9135;	
OX	[1]	
RN	SEQUENCE FROM N.A.	
RC	TISSUE=TESTIS;	
FX	MEDLINE=94130808; PubMed=8299561;	
RA	Nastluk K.L., Clayton D.F.;	
RT	"Seasonal and tissue-specific regulation of canary androgen receptor messenger ribonucleic acid."	
RL	Endocrinology 134:640-649(1994).	
CC	-1- SUBCELLULAR LOCATION(NUCLEAR). X	
CC	-1- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.	
DR	EMBL: L25901; AAA17402.1; .	
DR	HSP: P06536; IGLU.	
DR	InterPro: IPR000536; Hormone_rec_lig.	
DR	InterPro: IPR001723; Steroidhormone_receptor.	
DR	InterPro: IPR001628; zf-C4.	
DR	Pfam: PF00104; hormone_rec; 1.	
DR	Pfam: PF00105; zf-C4; 1.	
DR	PRINTS: PR00398; STRDHORMONER.	
DR	PRINTS: PR00047; STROIDFINGER.	
DR	SMART: SM00430; HOLI_1	
DR	SMART: SM00399; ZnF_C4; 1.	
KW	DNA-binding; Nuclear protein; Receptor; Transcription regulation;	
KW	Zinc-finger.	
FT	NON_TER 1	
FT	NON_TER 344	
FT	NON_TER 344	
SQ	SEQUENCE 344 AA; 39376 MW; 713676394FCBOB030 CRC64;	

  

	Query Match	34.1%	Score 1676;	DB 13;	Length 344;
	Best Local Similarity	90.4%;	Pred. No. 4.8e-118;		
	Matches 3il;	Conservative 20;	Mismatches 13;	Indels 0;	Gaps
QY	569 EASGCHYGALTCSCGKVFVKFAAEKGKYLCASNDCITDKFRKNPCPSLRKCYEAGM				628
Db	1 EASGCHYGALTCSCGKVFVKFAAEKGKYLCASNDCITDKFRKNPCPSLRKCYEAGM				630
QY	629 TLGAKLKLGNLKLOEGEASSSTTSPEETTQKLTVSHTEGYECQPIFNVLAEATPGV				678
Db	61 TLGAKLKLGNLKLAQDDIEGASSSTEQAAPLVVTRTDIGVECOPIFNVLAEATPGV				720
QY	689 VCAGHNDNQDPSFAALLSSLNELGEROLHVHWKAKALPGRNLHVDDOMAVLOYSWMGL				748
Db	121 VCAGHDNSQPDSFSNLSLTSELNERQLVVVWKAKALPGRNLHVDDQMSSIIQYSWMGL				800
QY	749 MYFAMGWRSFTNVNSRMLYFAPDLVFNEYMRHKSRMYSQCVNRHLISQBFGWLQITPQS				808
Db	181 MYFAMGWRSFTNVNSRMLYFAPDLVFNEYMRHKSRMYSQCIHRHLISQBFGWLQITPQG				840
QY	809 LCMKALLFSTIPVDGLNKOKFFEDELRRNYIKELDRLIAACKRNPTSCSRRFVOLTPLKD				868
Db	241 LCMKALLFFSIPTVDGLNKKQKLFDELRRMYIKELDRLIAACKRNPTSCSRRFVOLTPLKD				900
QY	869 SVQPIARELHQTFDDLTKSHMVSVDFPENMAEIISVQVPKILS				912
Db	301 SVTPIADLHQTFDDLTKKAHMVSVDYPENMAEIISVQVPKILS				944

RESULT	11	
ID	093245	
ID	093245	PRELIMINARY;
AC	093245;	PRT; 853 AA.
DT	01-NOV-1998	(TrEMBLrel. 08, Created)
DT	01-NOV-1998	(TrEMBLrel. 08, Last sequence update)
DE	01-JUN-2001	(TrEMBLrel. 17, Last annotation update)
DE	ANDROGEN RECEPTOR BETA,	
GN	AR-BETA.	
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;	
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.	
OX	NCBI_TaxID=8022;	
RN	[1]	



SEQUENCE FROM N.A.

Yamashita S.;  
"rainbow trout androgen receptor beta."  
Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
-1- SIMILARITY TO C4 TYPE STEROID RECEPTOR ZINC FINGER FAMILY.  
EMBL: AB012096; BAA32785.1; -  
HSP: P06536; LGDC.  
InterPro: IPR001103; Androgen\_recep.  
InterPro: IPR000536; Hormone\_rec\_lig.  
InterPro: IPR001628; zf-C4.  
Pfam: PF02156; Androgen\_recep; 1.  
Pfam: PF00104; hormone\_rec; 1.  
Pfam: PF00105; zf-C4; 1.  
PRINTS: P000047; STROIDFINGER.  
SMART: SM00430; HOLI; 1.  
SMART: SM00399; ZNF\_C4; 1.  
PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1.  
DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
zinc-finger.  
SEQUENCE 853 AA; 93776 MW; 65EFF5D3B36F4C4 CRC64;  
SO

	Query Match	33.4%;	Score 1639.5;	DB 13;	Length 853;
	Best Local Similarity	38.4%;	Pred. No. 8.7e-115;		
	Matches 386;	Conservative 129;	Mismatches 252;	Indels 239;	Gaps 30;
QY	1	MEVOLGLGRVTPRPSKTYRGAFOLFQSRYEVIQNPGPRHPHEAASAPPGASLLILLOQQ	60		
Db	1	MEIPVLGGVCD-SPNIVRFGFQNVHVKATL-----PSNTVTVTTLDFSSYSFMONK	55		
QY	61	QOQOQOQOQOQOQOQOQOQOQOQOQTSPPROQOQOQ-----EDGSPQAH-----RRGPTG	108		
Db	56	HPWEMROTNRQSPREITSSGTARNSEDEVKDDDISFSRTLESDDARRIHFAKSSCTGNKTG	115		
QY	109	YLVLDEEQP-----SQPGALCEHPERCVCPEPGAAVAASKGLPQOLPAAPPEDDSAA	162		
Db	116	FSSVNELDPNANGYSGSRGPGLACNTKKQCQC-----PAVPHHGVELS	159		
QY	163	PSTLSLLGPTFFGLSCSADLKLDLSENATMQLLOQOQOEAVSEGSSSGRAREASCAPTSS	222		
Db	160	PNSYARVA-----NSCS-----NSACT-----	176		
QY	223	SKDNYLGTTTISDNAKELCKAVSYSMLGYVE---ALEHLSP-----GQLRGDCMYAP	273		
Db	177	TISEARELCNVSVSLGITWDLNMENDLGENYAPSSANDOSQGNLFQ--	225		
QY	274	LLGVPPAVRPTECAPLAECCKGLLDDSAKSTEDTAETAYSPFKGYTKGLEGSILCGSGA	333		
Db	226	VPLNCSGA-----EENVSITEYK-----CPSER	249		
QY	334	AAGSSGTLELPSTLSLYKSGALDE-----AAAYQRDYNNFLALAGPPPppppp	382		
Db	250	NARPLEQSDTRVKMFKSSPANDITEVATMEHLUSSRHPTGQEPRLNKESDDPTSK-	305		
QY	383	PHPHARTKLENPLDYGSAWAAAACRYGDLASLHCA--GAAGPG-----	425		
Db	306	ETENSL-----STRASASCHFDPLPAHLAHSOTDPRDISSHVIPAHVCGTG	354		
QY	426	SCSPAAASSSNHTLTAELEGOLYGCPCGGGGGGGG	461		
Db	355	ETMEDKYADVLOQQOQYKIKYEIAISNEPATSWGSOYNINDNDMTQYCP-----	404		
QY	462	GGGGGGGGGGGGGEAGA-A-PYGTRPPOGLAQOESDFTAPDWYVPCGMVSRYVPSP	520		
Db	405	RQGNPNYSAGPSGFCINYEYER-GGGIVRRER--PTSEQWYPGMLGRMPV PNS	457		
QY	521	TCVRKSEKPMWDSYSGPYGDMRLTETARDHVLPIDITYFPDKTCLICGFASCHYGALTG	580		
Db	458	PYLKNEVGDWLDV---SYTDARFEGGRDHMFPEFEFFPPORTCLICADEASCHYGALTG	514		
QY	581	GSCKVFRAAEKGOKYLCAASRNDDCTIDKFRFNKNCPSCRKRCEYAGMTLGAARKLKLKLI	640		

Query Match	32.7%	Score 1604;	DB 6;	Length 303;
Best Local Similarity	99.0%;	Pred. No. 1e-112;		
Matches 300;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
564	LICGDEASGCHYGALTGCGSKVFFKRAAEGKQKYLCA	SRNDCTIDKFRKNCPSCLRKC	623	
1	LICGDEASGCHYGALTGCGSKVFFKRAAEGKQKYLCA	SRNDCTIDKFRKNCPSCLRKC	60	
624	YEAGNTLGARKLKLGNLQKEGEFASSTTSPRETTQKLT	VSHIEGYECQPIFNLVLEA	683	
61	YEAGNTLGARKLKLGNLQKEGEFASSTTSPREPAQKLT	VSHIEGYECQPIFNLVLEA	120	



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QY 684 IEPGVVACAGHNNOPDFAALLSSNLGELGRLVHVYVVKAKALPGFRNLHVDDQMAVIOY 743
DB 121 IEPGVVACAGHNNOPDFAALLSSNLGELGRLVHVYVVKAKALPGFRNLHVDDQMAVIOY 180
QY 744 SWMGLVFMGWRFTVNSRMLYFAPDLVFNEMRHKSRMYSOCVYMRHLSOEFGWLOI 803
DB 181 SWMGLVFMGWRFTVNSRMLYFAPDLVFNEMRHKSRMYSOCVYMRHLSOEFGWLOI 240
QY 804 TPQEFCLMKALLFSIIPVDGLKNOKFFDELNMNYIKELDRIIACKRKNPTSCSRFYQL 863
DB 241 TPQEFCLMKALLFSIIPVDGLKNOKFFDELNMNYIKELDRIIACKRKNPTSCSRFYQL 300
QY 864 TKL 866
DB 301 TKL 303

RESULT 13
O93497 PRELIMINARY; PRT; 769 AA.
AC O93497;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DE ANDROGEN RECEPTOR
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Chrysophrys.
OX NCBI_TaxID=811;
RN [1]
RP SEQUENCE FROM N.A.
RA Tounata K., Toyohata H.
RT "Red seabream androgen receptor."
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL: AB017158; BAA33451.1; -.
DR HSSP: P06536; IRGD.
DR InterPro: IPR001103; Androgen_recep.
DR InterPro: IPR000536; Hormone_rec_lig.
DR InterPro: IPR001628; zf-C4.
DR Pfam: PF02166; Androgen_recep.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STROIDFINGER.
DR SMART: SM00430; HOLI; 1.
DR SMART: SM00399; ZnF_C4; 1.
DR PROSITE: PS00031; NUCLEAR RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 769 AA; 86081 MW; 9305C627DBE42062 CRC64;

Query Match 32.7%; Score 1604; DB 13; Length 769;
Best Local Similarity 43.9%; Pred. No. 3.5e-112;
Matches 363; Conservative 79; Mismatches 171; Indels 214; Gaps 23;

QY 205 SEGSSSGRAFEASCA-PTSSKDNYL----- 228
DB 46 STGAGRMREADNADPNTYESGHMPLVCDMEKHCCQTAAAPQBELFNADCRVGDSSRF 105
QY 229 GGTSTISDNKELCKAVSVSMGLGV-----ALEHLSPEQLRGDCWVAPLLGVPP 279
DB 106 SACATISSETARELCKAVSVSLGLAMESNDPMDAALSOCAANDLGRLEYLFG----- 158
QY 280 AVRPTPCAPLAECKGSLDDSAKSTEDTAEYSPFGKGYTKGEGESLGCSSRAAGSSG 339
DB 159 -----VGAAPLS-CPGA-----QAAYSEYKCPPEPLHGHK----- 188
QY 340 TLELPSTLSLYKSGALDEAAAYQSR-----DYNFPALAGPPPPPPPPHARIKL 391

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DB 189 --QQOQLMDNFKS---SETGAHLQHLTSTRTPYDEHNFTLCKAEDLTPEHTAQD----- 238
QY 392 ENPLDYGSAAAAAACQRYGDLASLHGAGAAGPGS---GSPSAAASSSWHTLFTAEGQ 447
DB 239 -----SVRAAACPY-----AQSLPGNMAHFGSP--APERFW----- 269
QY 448 LYGPCGGGGGGG-----GGGGGGGGG----- 469
DB 270 LYRPPDEAGDFGVMSRFRVTSYQPEQYSVKIKGEDTESAGALWGNVTFNDRYNSQCV 329
QY 470 -----GGGGGGGAGAVAPYGYTRPPQGLAQESDFAPDVVYVPGMVSRVPPSPTCV 523
DB 330 GPRQCMNAHSTGANSALCHPY-----ERSVARPEHWYPGGML-RSPYPNSSYV 376
QY 524 KSEMGPMDSYSGPYCDMRLETARDHVLPIDYFPPQKTCICGDEASGCHYGALTCGSC 583
DB 377 KSEVGWLDV---PYSDFRDSSEHMFTEFFPAQRMCLICDEASGCHYGALTCGSC 433
QY 584 KVFRAAEGKQKYLCAASNDCTIDKFRKNCPCSLRLEKCYEAGMTLGARKLKLGNLK- 642
DB 434 KVFRAAEGKQKYLCAASKNDCTIDKLRKNCPCSLRLEKCYEAGMTLGARKLKLGNLK 493
QY 643 -----LQEEGASSTTSPTETTKLTVSHIEGYEQPIFLNVLEAIEPCVVCAGHDNN 696
DB 494 SDEHPLQEPAEVMPNISPKSGLS-----FNSQVFLNVLESTEPVNVNAGHDY 543
QY 697 QPDSFAALLSSNLGELGRLVHVYVVKAKALPGFRNLHVDDQMAVIOYSWMGLVMFAMGW 756
DB 544 QPDSAAATLLTSLNELGERQLVVKVAKGLPGFRNLHVDDQMTVIOHSMGMVAVFGLGWR 603
QY 757 SFTNYSRMLYFAPDLVFNEMRHKSRMYSOCVYMRHLSOEFGWLOITPOEFLCMKALL 816
DB 604 SYKNVNGRMLYFAPDLVFNEMRHMISTMYEHCIMRHLSEFLLQLTQEEFLCMKALL 663
QY 817 FSLIPVGLKNOKFFDELNMNYIKELDRIIACKRKNPTSCSRFYQLTKLLDSVQPIARE 876
DB 664 FSLIPVGLKNOKFFDELNMNYIKELDRIIACKRKNPTSCSRFYQLTKLLDSVQPIARE 921
QY 877 LHQFTFDLLIKSHMV--SVDPFPMMAEIIISVQPKILSGKVKPIYH 921
DB 722 LHQFTFDLVQAQSLPTKVSFPEMIGELIISVHVPKILAGLAKPILPH 768

RESULT 14
O9PWG5 PRELIMINARY; PRT; 797 AA.
AC O9PWG5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ANDROGEN RECEPTOR-BETA
GN AR-BETA.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillioidei;
OC Anguillidae; Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA MEDLINE=99395076; PubMed=10464240;
RA Ikeuchi T., Todo T., Kobayashi T., Nagahama Y.;
RT "cDNA cloning of a novel androgen receptor subtype."
RL J. Biol. Chem. 274:25203-25206 (1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL: AB025361; BAA83805.1; -.
DR HSSP: P06536; IRGD.
DR InterPro: IPR001103; Androgen_recep.
DR InterPro: IPR000536; Hormone_rec_lig.
DR InterPro: IPR001723; Steroidhormone_receptor.
DR InterPro: IPR001628; zf-C4.

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QY 882 FDLIKSHMV--SVDEPEMAEIIISVQPKILSGKVKPIYFH 921  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 755 FDLFVQAQSLHTKVNFPPEMAEIIISVHVPRILAGMAKPILFH 796

RESULT 15  
 O93244 PRELIMINARY; PRT; 854 AA.  
 ID O93244  
 AC O93244;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE ANDROGEN RECEPTOR ALPHA.  
 GN AR-ALPHA.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Ramashita S.  
 RT "Rainbow trout androgen receptor alpha."  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -!- SIMILARITY: 40 C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.  
 DR EMBL; AB012095; BAA32784.1;  
 DR HSP; P06536; 1GDC.  
 DR InterPro; IPR001103; Androgen\_recep;  
 DR InterPro; IPR000536; Hormone\_rec\_lig.  
 DR InterPro; IPR001628; zf-C4.  
 DR Pfam; PF02166; Androgen\_recep; 1.  
 DR Pfam; PF00104; hormone\_rec; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; Znf.C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
 SQ ZINC-finger. 854 AA; 96237 MW; 9F123B27874B0728 CRC64;

Query Match 31.7%; Score 1556; DB 13; Length 854;  
 Best Local Similarity 39.8%; Pred. No. 1.6e-108;  
 Matches 386; Conservative 121; Mismatches 298; Indels 164; Gaps 31;

QY 1 MEVOLGLGRVYPPRPKTYRGAPNLFQSVREVIQNGPRHPEAASAPPGLLQLQQ 60  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 1 MEIPVGLGVCD-STNLVFRGPQNVFHVQALPSN--TTVTESLDFCSSKFSFL----- 52  
 QY 61 QQQ 120  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 53 -ONKQPMEMKQASQSRKEIWSGTARNSDIEVREDS-----VGF-----SR 94  
 QY 121 QSALECHPERGCVPEPGAAVAASKGLPOOLPAPPPEDDSDAPSTLSLLGPTFPGLSSCS 180  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 95 TLESVACRIH-----FAKSSKGNKAGFSLNESDN-----PANEGSCR 134  
 QY 181 ADLKDILSEASTMOLQQQQQEAWS-EGSSSGRAREASGAPTSSKDNVLCGTSTISDNK 239  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 135 SG-----QQVSNTF--QQSCOPSVSHHGNELNINSEACVASSCSS-----SACSTISKAR 183  
 QY 240 ELCKAVSVSMGLGVEALE--HLSP-----GEQLRGDCMYAPLLGVPPAVRPTCAPLA 290  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 184 ELCNVAVSLSGLTMDANEMTDLGNHAPSSVNHQSOGNVLF-----VPLL 229  
 QY 291 ECKGSLDDSDAGKSTEDTAESYSPKGGYTKCELESISGCSAAAGSGGTLEPSTLSLY 350  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 230 KCSG-----AGENVSIT-EYTCPSERNAPQLQSDKOLVEMFORSFANDLTKVATIQHL 282  
 QY 351 KSG-----ALDAAAYOSRD-----YYNFPLALAGPPPPPPPPH----- 384  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

DR Pfam; PF02166; Androgen\_recep; 1.  
 DR Pfam; PF00104; hormone\_rec; 1.  
 DR Pfam; PF00105; zf-C4; 1.  
 DR PRINTS; PR00398; STRDHORMONER.  
 DR PRINTS; PR00047; STROIDFINGER.  
 DR SMART; SM00430; HOLI; 1.  
 DR SMART; SM00399; Znf.C4; 1.  
 DR PROSITE; PS00031; NUCLEAR\_RECEPTOR; 1.  
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;  
 SQ ZINC-finger. 797 AA; 89924 MW; CF1D5F21EEEA5691 CRC64;

Query Match 32.68%; Score 1600; DB 13; Length 797;  
 Best Local Similarity 43.08%; Pred. No. 7.4e-112;  
 Matches 379; Conservative 105; Mismatches 220; Indels 178; Gaps 27;

QY 112 LDEEQ-----PSQPOS-ALECHPERGCVPEPGAAVAASKGLPOOLPAPPPEDDSDAAP 163  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 21 LDELEQADSANFPMPQPEAEARRIHFTKS-----SDSKGDSIL-----EPDNAQE 66  
 QY 164 STLSLGLPTPGLSSCADLKILSEASTMOLQQQQQEAWS-EGSSSGRAREASGAPTSS 223  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 67 NA---YCPFLSLDHDCCTDKRSLSLTAPNRREINPHSDACVNSCSESA----- 113  
 QY 224 KDNVLGCTSTISDNKELKAVSVSMGLGVEALEHLSLSP-----GEQLRGDCMY-APL 274  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 114 -----CITISETARELKAVSVSLGNMDSNEMNEPCHNLASSLGLDLKFMFEVFF 166  
 QY 275 LGVPPAVRPTPCAPLAECKGSLDDSDAGKSTEDTAESYSPKGGYTKGLEGE----- 325  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 167 LG---SSGTOESYPRAYEACARLHD--GOLLONDELSCMKFTHVQGLTNEVAPSHLSS 221  
 QY 326 -----SLGSSGSAAGSSGTLTLE-----LPSTLSLYKSGALDEAAA 360  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 222 YSNWDTQETRLNAETETSASKEQASCTMDAARSGFCOPDOLLPTTLAQYSQ--IDPLSM 279  
 QY 361 ----YQSRDYNTPLALAGPPPPPPPHPHA-----RIKENPLDY--GSAA 402  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 280 GRNFRSQFFYK-TLALANAV-----EHAERYVDSSIQYSPKIKTENLQNSGGSW- 331  
 QY 403 AAAQCRYGLDASLHGAGAAGPGSGPSAAASSSWHTLFTAEEOGLYPCGCGGGGGGGG 462  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 332 --DHQRYNE-----NHSQYGPSRHGLHPYC----- 356  
 QY 463 GGGGGGGGGGGGGEAGAVAPYGYTRPPQCLAGQESDFTAPDVMYPGMVSRVYPSPTC 522  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 357 -----TETNNQVVEFFDYQ---GGGLLPDRSASESWFFPGGMLSKMPTNLPC 403  
 QY 523 VKSEMGPMWDSYSGPYD-MRELTARDHVLPIIDYFPQKTCILICGDEASGCHYGALTGC 581  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 404 LKTEVADMLEV---PCSDRMLEGGREHVPMEFFPPORTCLICADEASGCHYGALTGC 460  
 QY 582 SCKVFKRAAECKQKYLCAASNDCTIDKFRKNCPCSLKCKYEAAGTLCARKLKLGNL 641  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 461 SCKVFKRAAECKQKYLCAASNDCTIDKLRKNCPCSLKCKCFEAGTLCARKLKLGQL 520  
 QY 642 KLOEAGEASSTSPTEETTKLTVSHIEGYEQPIFLNLEATEPGVVCAGHDNNQPDSE 701  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 521 KPPDELPTQAPTDALQISPKPGLS-----FPTQSVFLNILESIEPEVYNAGHDYQGTDSA 576  
 QY 702 AALLSLSNELGRQLVHVWAKALPGFRNLHVDQMAVIOYSWMGLMVFAMGWSFTNV 761  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 577 ATLLTSLNELGRQLFKVVKWAKGLPGFRNMHVDDQMTVIOHAMVMYVFAFGMRYSKNV 636  
 QY 762 NSRMLYFADPLVFNERYMRHKSVMYSOCVYMRHLQSQFGLQITPOEFLCMKALLFSIIP 821  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 637 NARMLYFADPLVFNDRMRVMSVYEHCIEMRMHSGOEFVLLQVTHQEFELCMKALLFSIIP 696  
 QY 822 VDLGNKQKFFDELRMNMYIKELDRIIACKRNKPTSCSRFYOLTKLLDSVQPIARELHQFT 881  
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :  
 Db 697 VEGLLKQKQYFDDLRLNTYINELDRILNCSRK--TNCRSORFIQILTRIMDSLOPIVKKLHQFT 754

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Db 283 SSGHPCWDKQEFRLNENRDPTSKETDHELTCAKRSYHFDQLL-----PAHLAHF 334
QY 385 -----PHARIKLEPLDYGSAAWAAAQCRYGD-LASLHGAGAGPGSGSPSAASS 436
Db 335 SOTETDRNSSHVYKPAHVE--TGETMEDYADYLOOQYSVKIKYEFNRHNLPEPS 392
QY 437 W--HTLFTAEQOLYPCGCGGGGGGGGGGGGGGAGAVAPYGYTRPPQCLA 494
Db 393 WDFQYRNDNDNTQYGL-----NSYIAGPDSALICNPHEYER-GGGLV 434
QY 495 GQESDFTAPDVVPGGMYSRVPYPSPTCVKSEMGPMDSYSGPYGDMRLETARDHVLPI 554
Db 435 RRER--PTEQWYPMGLRMPYNSPCIKNEVG---DSLDVSYTDARFEGGSDHMYPME 489
QY 555 YFPPQKTCLICGDEASGCHYGALTCGCKVFFKRAEGKOKYLCASRNDCTIDKFRKN 614
Db 490 FFFPORTCLICAEASGCHYGALTCGCKVFFKRAEGKOKYLCASRNDCTIDKFRKN 549
QY 615 CPSCRLRKCYEAGMTLGARKLKLGNLKLQEEGEASSTTSPTETTKLTAVSHIEGYEQ 674
Db 550 CPSCRLRRCFAGMTLGTGRKLKIVOLKSPED--LPTQGT-DTIQGVSPQSLSEHSQ 606
QY 675 PIFNLVLEAIEPPGVVACAGHNNQPOSAALLSSNLGELGRLVHVVKWAKALPGFRNLHV 734
Db 607 LVFLNILESIBFVYVHAGHOCQDPSAALLTSLNELGERQLVVKWAKALPGFRNLHV 666
QY 735 DDOMAVIOYSWMLMVFAMGRSFTNYSRMLYFAPDLVFNERYMHKSRMYSOCVRRHL 794
Db 667 DQMTVIOHSMGYMVFGLGWRSYKNANCRLLYFAPDLVFNDRHMHSSMFDHCIRROL 726
QY 795 SOEFGWITPOEFLCMKALLFSIIPVGLKNOKFFDELBMNYIKELDRIIACKRKNT 854
Db 727 SOEVLVQVTOEEFLCMKALLFSIIPVGLKSOKYFDELRLTYINELGRVINYGRK--S 784
QY 855 SCSRRFYOLTKLDSVOPIARELHQFTFDLLIKSHMV--SVDFFPENMAEIIISVQPKILS 912
Db 785 NCSORLYQLRLMDSLQPVVVKLQQTFTDLFVQAQSLPTKVNFPEMIAELISVHLPKILA 844
QY 913 GKVKPIYFH 921
Db 845 GLAKPILFH 853

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Job time: 365 sec

